FIGURE 1

```
  1  GAATTCGGCACGAGAGCACTCCAAGCACTGCTGTCTTCTCACAGAGTCTTGAAGCCAGAG

 61  CAGCGCCAGG ATG TCA CGG GAG CTG GCC CCA CTG CTG CTT CTC CTC
-20             Met Ser Arg Glu Leu Ala Pro Leu Leu Leu Leu Leu

107  CTC TTC ATC CAT AGC GCC CTG GCC ATG AGG ATC TGT TCC TTC AAC
 -8  Leu Ser Ile His Ser Ala Leu Ala Met Arg Ile Cys Ser Phe Asn
                                    ▲

152  GTC AGG TCC TTT GGG GAA AGC AAG CAG GAA GAC AAG AAT GCC ATG
  8  Val Arg Ser Phe Gly Glu Ser Lys Gln Glu Asp Lys Asn Ala Met

197  GAT GTC ATT GTG AAG GTC ATC AAA CGC TGT GAC ATC ATA CTC GTG
 23  Asp Val Ile Val Lys Val Ile Lys Arg Cys Asp Ile Ile Leu Val

242  ATG GAA ATC AAG GAC AGC AAC AAC AGG ATC TGC CCC ATA CTG ATG
 38  Met Glu Ile Lys Asp Ser Asn Asn Arg Ile Cys Pro Ile Leu Met

287  GAG AAG CTG AAC AGA AAT TCA AGG AGA GGC ATA ACG TAC AAC TAT
 53  Glu Lys Leu Asn Arg Asn Ser Arg Arg Gly Ile Thr Tyr Asn Tyr

332  GTG ATT AGC TCT CGG CTT GGA AGA AAC ACA TAT AAA GAA CAA TAT
 68  Val Ile Ser Ser Arg Leu Gly Arg Asn Thr Tyr Lys Glu Gln Tyr

377  GCC TTT CTC TAC AAG GAA AAG CTG GTG TCT GTG AAG AGG AGT TAT
 83  Ala Phe Leu Tyr Lys Glu Lys Leu Val Ser Val Lys Arg Ser Tyr

422  CAC TAC CAT GAC TAT CAG GAT GGA GAC GCA GAT GTG TTT TCC AGG
 98  His Tyr His Asp Tyr Gln Asp Gly Asp Ala Asp Val Phe Ser Arg

467  GAG CCC TTT GTG GTC TGG TTC CAA TCT CCC CAC AGT GCT GTC AAA
113  Glu Pro Phe Val Val Trp Phe Gln Ser Pro His Thr Ala Val Lys

512  GAC TTC GTG ATT ATC CCC CTG CAC ACC ACC CCA GAG ACA TCC GTT
128  Asp Phe Val Ile Ile Pro Leu His Thr Thr Pro Glu Thr Ser Val

557  AAG GAG ATC GAT GAG TTG GTT GAG GTC TAC ACG GAC GTG AAA CAC
143  Lys Glu Ile Asp Glu Leu Val Glu Val Tyr Thr Asp Val Lys His

    CGT TGG AAG GCG GAG AAT TTC ATT TTC ATG GGT GAC TTC AAT GCC
156 Arg Trp Lys Ala Glu Asn Phe Ile Phe Met Gly Asp Phe Asn Ala

647  GGC TGT AGC TAC GTC CCC AAG AAG GCC TGG AAG AAC ATC CGC TTG
173  Gly Cys Ser Tyr Val Pro Lys Lys Ala Trp Lys Asn Ile Arg Leu

692  AGG ACT GAC CCC AGG TTT GTT TGG CTG ATC GGG GAC CAA GAG GAC
188  Arg Thr Asp Pro Arg Phe Val Trp Leu Ile Gly Asp Gln Glu Asp

737  ACC ACG GTG AAG AAG AGC ACC AAC TGT GCA TAT GAC AGG ATT GTG
203  Thr Thr Val Lys Lys Ser Thr Asn Cys Ala Tyr Asp Arg Ile Val

782  CTT AGA GGA CAA GAA ATC GTC AGT TCT GTT GTT CCC AAG TCA AAC
218  Leu Arg Gly Gln Glu Ile Val Ser Ser Val Val Pro Lys Ser Asn

827  AGT GTT TTT GAC TTC CAG AAA GCT TAC AAG CTG ACT GAA GAG GAG
233  Ser Val Phe Asp Phe Gln Lys Ala Tyr Lys Leu Thr Glu Glu Glu

872  GCC CTG GAT GTC AGC GAC CAC TTT CCA GTT GAA TTT AAA CTA CAG
248  Ala Leu Asp Val Ser Asp His Phe Pro Val Glu Phe Lys Leu Gln

    TCT TCA AGG GCC TTC ACC AAC AAT AAA AAA TCT GTC ATT CTA AGG
263 Ser Ser Arg Ala Phe Thr Asn Asn Lys Lys Ser Val Ile Leu Arg

    AAG AAA ACA AAG AGT AAA CAT TCT TA GATTCAA GGTGTCATTTATTAAT
278 Lys Lys Thr Lys Ser Lys Arg Ser

1013 CCATTTCTTCTTTAAATAAAC TCTTTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
```

FIGURE 2

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hu.LS.DNase     1  M R I C S F N V R S F G E S K Q E D K N A M D V I V K V I K C D I I L V M E I K D S N N R I C P I
hu.DNaseI       1  L K I A A F N I Q T F G E T K M S N A T L V S Y I V Q I L S R Y D I A L V Q E V R D S H L T A V G K
                                                        *

hu.LS.DNase    51  L M E K L N R N S R R G I T Y N Y V I S S R L G R N T Y K E Q Y A F L Y K E K L V S V K R S Y H Y H
hu.DNaseI      51  L L D N L N Q D A P D - - T Y H Y V V S E P L G R N S Y K E R Y L F V Y R P D Q V S A V D S Y Y Y D

hu.LS.DNase   101  D - Y Q D G D A D V F S R E P F V V W F Q S P H T A V K D F V I P L H A A P G D A V A E I D A L Y
hu.DNaseI      99  D G C E P C G N D T F N R E P A I V R F F S R F T E V R E F A I V P L H A A P G D A V A E I D A L Y
                           *                                                              ◄

hu.LS.DNase   150  E V Y T D V K H R W K A E N F I F M G D F N A G C S Y V P K K A W K N I R L R T D P R F V W L I G D
hu.DNaseI     149  D V Y L D V Q E K W G L E D V M L M G D F N A G C S Y V R P S Q W S S I R L W T S P T F Q W L I P D

hu.LS.DNase   200  Q E D T T V K K S T N C A Y D R I V L R G Q E I V S S V V P K S N S V F D F Q K A Y K L T E E E A L
hu.DNaseI     199  S A D T T A - T P T H C A Y D R I V V A G M L L R G A V V P D S A L P F N F Q A A Y G L S D Q L A Q
                                          ◄

hu.LS.DNase   250  D V S D H F P V E F K L Q S S R A F T N S K K S V T L R K K T K S K R S
hu.DNaseI     248  A I S D H Y P V E V M L K
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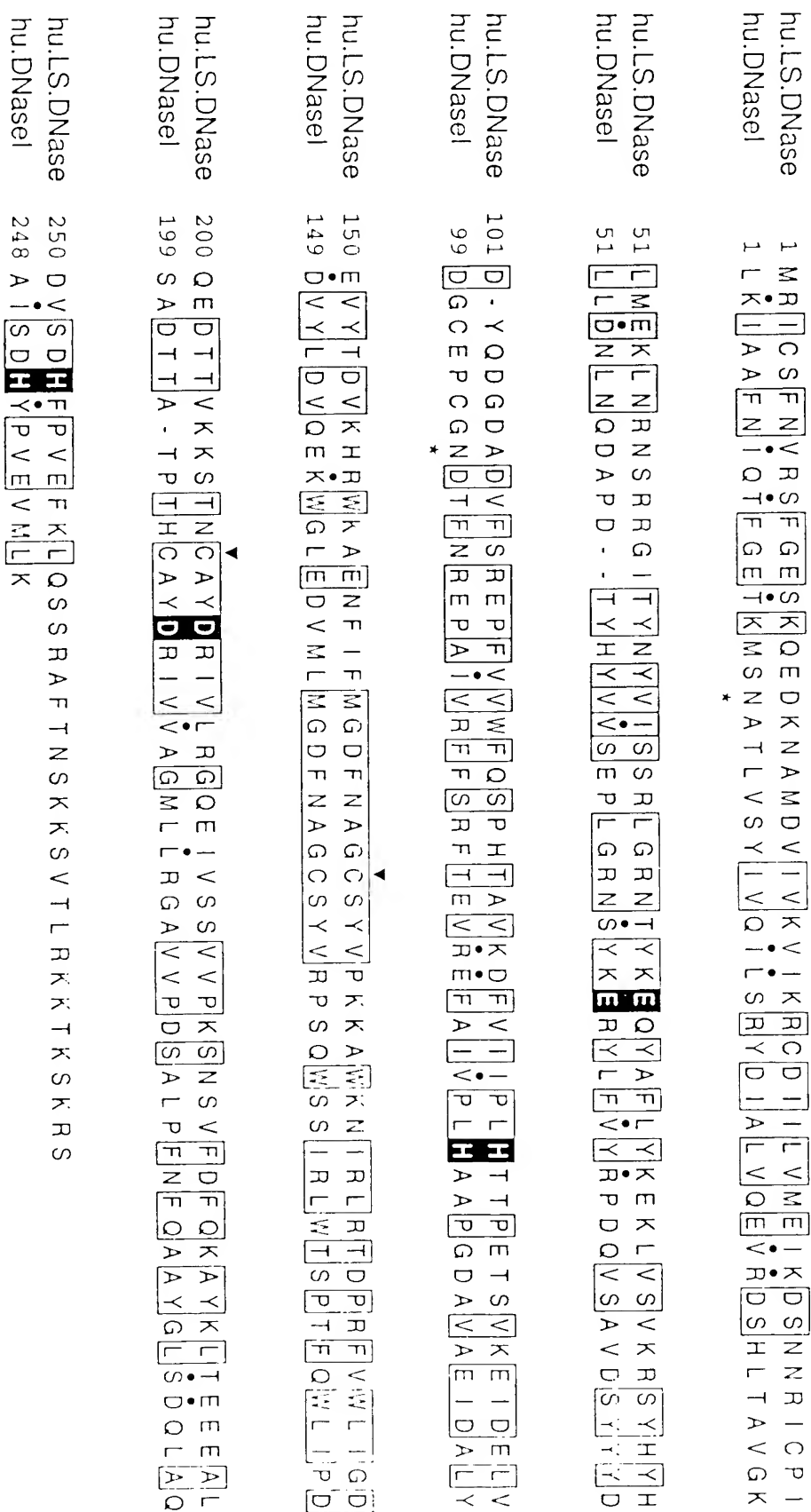
FIGURE 3

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   1  GAATTCCGGCTCATTACCTTCATTTCCTTGGGGATTGAAACGCGTGATGG
  51  TGAGTTCCTCAGAGAAGTGAAAGTGACCTAGAGGGATCCAGTAATTCCTG
 101  TTATCAGCCTGCTTTATAAGTCAGTGAGCCAGGCACTGTCTTCATCCAGC
 151  CTGAAGTCCCAGGAGTGCAAAGATGTCCCTGCACCCAGCTTCCCCACGCC
                                    ▲
 201  TGGCCTCCCTGCTGCTCTTCATCCTTGCCCTCCATGACACCCTGGCCCTA
 251  AGGCTCTGCTCCTTCAATGTGAGGTCCTTTGGAGCGAGCAAGAAGGAAAA
 301  CCATGAAGCCATGGATATCATTGTGAAGATCATCAAACGCTGTGACCTTA
 351  TACTGTTGATGGAAATCAAGGACAGCAGCAACAACATCTGTCCCATGCTG
 401  ATGGAGAAGCTGAATGGAAATTCACGAAGAAGCACAACATACAACTATGT
 451  GATTAGTTCTCGACTTGGAAGAAACACGTACAAAGAGCAGTATGCCTTCG
 501  TCTACAAGGAGAAGCTGGTGTCTGTGAAGACAAAATACCACTACCATGAC
 551  TATCAGGATGGAGACACAGACGTGTTTTCCAGGGAGCCCTTTGTGGTTTG
 601  GTTCCATTCCCCCTTTACTGCTGTCAAGGACTTCGTGATTGTCCCCTTGC
 651  ACACAACTCCCGAGACCTCCGTTAAAGAGATAGATGAGCTGGTCGATGTC
 701  TACACGGATGTGAGAAGCCAGTGGAAGACAGAGAATTTCATCTTCATGGG
 751  TGATTTCAACGCCGGCTGTAGCTATGTCCCCAAGAAGGCCTGGCAGAACA
 801  TTCGTTTGAGGADGGACCCCAAGTTTGTTTGGCTGATTGGGGACCAAGAG
 851  GACACTACGGTCAAGAAGAGTACCAGCTGTGCCTATGACAGGATTGTGCT
 901  TTGTGGACAAGAGATAGTCAACTCCGTGGTTCCCCGTTCCAGTGGCGTCT
 951  TTGACTTTCAGAAAGCTTATGACTTGTCTGAGGAGGAGGCCCTGGATGTC
1001  AGTGATCACTTTCCAGTTGAGTTTAAGCTACAGTCTTCAAGGGCCTTCAC
1051  CAACAACAGAAAATCTGTTTCTCTCAAAAAGAGAAAAAAGGCAATCGCT
1101  CCTAGGTATCACGCTCCGGAATTC
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